

09/744926 #3

02 Rec'd PCT/PTO 30 JAN 2001

SEQUENCE LISTING

<110> FROHBERG, Claus

<120> NUCLEIC ACID MOLECULES ENCODING AN ALPHA-GLUCOSIDASE, PLANTS WHICH
SYNTHESIZE A MODIFIED STARCH, THE GENERATION OF THE PLANTS, THEIR USE, AND THE
MODIFIED STARCH

<130> 514413-3865

<150> PCT/EP99/05536

<151> 1999-07-31

<150> DE 198 36 097.5

<151> 1998-07-31

<160> 2

<170> PatentIn version 3.0

<210> 1

<211> 2272

<212> DNA

<213> Solanum tuberosum

<220>

<221> CDS

<222> (135)..(2180)

<223> coding sequence of alpha-glucosidase

<400> 1	60
cgaatacgaa taaccgacgc taaccatcaa cgatggaaag tgccggaaga aattctccac	
cgtccaccac cgccgtcgcc gccgtcaacc tccaaactcct catcagaaaa ccactccccca	120
attaccctct ctaa ccc aaa ctc aga cct aga gtt cac cct tca caa cac	170
Pro Lys Leu Arg Pro Arg Val His Pro Ser Gln His	
1 5 10	
cat ccc att cag ctt cac cgt ccg ccg gcg ctc cac cgg gga tac tct	218
His Pro Ile Gln Leu His Arg Pro Pro Ala Leu His Arg Gly Tyr Ser	
15 20 25	
ttt cga tac ttc gcc gga gtt agt cat ggg gtt ttg ctt ctg agt agc	266
Phe Arg Tyr Phe Ala Gly Val Ser His Gly Val Leu Leu Ser Ser	
30 35 40	
aat ggc atg gat att gtg tat acg ggt gat agg att agt tac aag gtg	314
Asn Gly Met Asp Ile Val Tyr Thr Gly Asp Arg Ile Ser Tyr Lys Val	
45 50 55 60	
att gga ggg tta att gat ttg tat ttc ttt gcc gga cct tcg ccg gaa	362
Ile Gly Gly Leu Ile Asp Leu Tyr Phe Phe Ala Gly Pro Ser Pro Glu	
65 70 75	
atg gtg gtg gat cag tat act cag ctt att ggt cgt cct gct gct atg	410

Met Val Val Asp Gln Tyr Thr Gln Leu Ile Gly Arg Pro Ala Ala Met			
80	85	90	
cca tat tgg tct ttc gga ttt cac caa tgc cggtt ggt tac aag aat			458
Pro Tyr Trp Ser Phe Gly Phe His Gln Cys Arg Trp Gly Tyr Lys Asn			
95	100	105	
att gat gat gtt gaa ctg gta gtg gat agt tat gca aag tct aga ata			506
Ile Asp Asp Val Glu Leu Val Val Asp Ser Tyr Ala Lys Ser Arg Ile			
110	115	120	
ccg ctg gag gtt atg tgg act gat att gat tac atg gat ggt ttt aag			554
Pro Leu Glu Val Met Trp Thr Asp Ile Asp Tyr Met Asp Gly Phe Lys			
125	130	135	140
gac ttc aca ctc gat cca gtt aac ttc cca ctg gag cggtt gta att ttt			602
Asp Phe Thr Leu Asp Pro Val Asn Phe Pro Leu Glu Arg Val Ile Phe			
145	150	155	
ttt ctc agg aag ctt cat cag aat gat cag aaa tat gta cta ata gta			650
Phe Leu Arg Lys Leu His Gln Asn Asp Gln Lys Tyr Val Leu Ile Val			
160	165	170	
gat cca gga att agc atc aac aat aca tat gac acc tat agg aga ggc			698
Asp Pro Gly Ile Ser Ile Asn Asn Thr Tyr Asp Thr Tyr Arg Arg Gly			
175	180	185	
atg gaa gca gat gtc ttc ata aaa cgc gat aat atg ccc tac caa ggg			746
Met Glu Ala Asp Val Phe Ile Lys Arg Asp Asn Met Pro Tyr Gln Gly			
190	195	200	
gtt gtt tgg cca ggg aat gtt tat tat cct gat ttt cta aat cca gct			794
Val Val Trp Pro Gly Asn Val Tyr Tyr Pro Asp Phe Leu Asn Pro Ala			
205	210	215	220
act gaa gta ttt tgg aga aat gaa att gag aag ttc cag gat ctc gta			842
Thr Glu Val Phe Trp Arg Asn Glu Ile Glu Lys Phe Gln Asp Leu Val			
225	230	235	
cct ttt gat ggc ctg tgg ctt gac atg aat gaa ttg tca aac ttc ata			890
Pro Phe Asp Gly Leu Trp Leu Asp Met Asn Glu Leu Ser Asn Phe Ile			
240	245	250	
act tcc cct cct aca cca tca tct acc ttt gat gat cct ccc tac aag			938
Thr Ser Pro Pro Thr Pro Ser Ser Thr Phe Asp Asp Pro Pro Tyr Lys			
255	260	265	
ata aac aac tct ggc gat cac ttg ccc atc aat tat aga aca gtt cca			986
Ile Asn Asn Ser Gly Asp His Leu Pro Ile Asn Tyr Arg Thr Val Pro			
270	275	280	
gcc act tct aca cat ttt ggt gat aca atg gag tat aat gtc cat aac			1034
Ala Thr Ser Thr His Phe Gly Asp Thr Met Glu Tyr Asn Val His Asn			
285	290	295	300
ctt tat gga tta ctt gaa tct aga gcc act tat agt gca ttg gtt aat			1082
Ley Tyr Gly Ley Ley Glu Ser Arg Ala Thr Tyr Ser Ala Ley Val Asn			

305	310	315	
gtc act ggt aaa agg cca ttc att ctt gta aga tca act ttt ctt ggc Val Thr Gly Lys Arg Pro Phe Ile Leu Val Arg Ser Thr Phe Leu Gly 320	325	330	1130
tct ggc aga tac acg tca cat tgg act gga gat aat gct gct acc tgg Ser Gly Arg Tyr Thr Ser His Trp Thr Gly Asp Asn Ala Ala Thr Trp 335	340	345	1178
aac gat ttg gca tac tcc att cct act atc ttg agc ttt gga ttg ttt Asn Asp Leu Ala Tyr Ser Ile Pro Thr Ile Leu Ser Phe Gly Leu Phe 350	355	360	1226
gga att cca atg gtt gga gct gat ata tgt ggt ttt tca agt aac act Gly Ile Pro Met Val Gly Ala Asp Ile Cys Gly Phe Ser Ser Asn Thr 365	370	375	1274
act gaa gag ctt tgc cgc cgc tgg att cag ctt gga gca ttc tat cca Thr Glu Glu Leu Cys Arg Arg Trp Ile Gln Leu Gly Ala Phe Tyr Pro 385	390	395	1322
ttt gca aga gac cac tct gct aag gac aca acc ccc caa gag ctc tat Phe Ala Arg Asp His Ser Ala Lys Asp Thr Thr Pro Gln Glu Leu Tyr 400	405	410	1370
agt tgg gat tca gtt gct gca gca gcc aag aaa gtc ctt ggg ctc cga Ser Trp Asp Ser Val Ala Ala Ala Lys Lys Val Leu Gly Leu Arg 415	420	425	1418
tat cag tta ctt cca tac ttt tat atg ctt atg tac gag gca cat ata Tyr Gln Leu Leu Pro Tyr Phe Tyr Met Leu Met Tyr Glu Ala His Ile 430	435	440	1466
aaa ggg act ccc att gca cga ccc ctc ttc ttc tct ttc cct caa gat Lys Gly Thr Pro Ile Ala Arg Pro Leu Phe Phe Ser Phe Pro Gln Asp 445	450	455	1514
gcc aag aca ttt gat atc agc aca cag ttc ctt ctc ggt aaa ggt gtc Ala Lys Thr Phe Asp Ile Ser Thr Gln Phe Leu Leu Gly Lys Gly Val 465	470	475	1562
atg atc tca cct ata ctt aag caa gga gca acc tct gtt gat gca tat Met Ile Ser Pro Ile Leu Lys Gln Gly Ala Thr Ser Val Asp Ala Tyr 480	485	490	1610
ttc cct gct gga aac tgg ttt gac ctc ttc aat tac tct cgc tct gtg Phe Pro Ala Gly Asn Trp Phe Asp Leu Phe Asn Tyr Ser Arg Ser Val 495	500	505	1658
agt ttg aat caa gga aca tat atg aca ctt gac gca cca cca gat cat Ser Leu Asn Gln Gly Thr Tyr Met Thr Leu Asp Ala Pro Pro Asp His 510	515	520	1706
ata aat gta cat gtt cgt gaa ggg aac ata ttg gtc atg caa ggg gaa Ile Asn Val His Val Arg Glu Gly Asn Ile Leu Val Met Gln Gly Glu 525	530	535	1754
			540

gca atg aca aca caa gct gct cag agg act gca ttc aaa ctc ctt gtc Ala Met Thr Thr Gln Ala Ala Gln Arg Thr Ala Phe Lys Leu Leu Val 545 550 555	1802
gtg ctg agc agc agc aaa aac aac aca gga gaa cta ttt gtg gac gat Val Leu Ser Ser Ser Lys Asn Ser Thr Gly Glu Leu Phe Val Asp Asp 560 565 570	1850
gac gat gag gtg cag atg gga aga gag gga ggg agg tgg acg cta gtt Asp Asp Glu Val Gln Met Gly Arg Glu Gly Arg Trp Thr Leu Val 575 580 585	1898
aag ttt aac agc aat atc att ggc aat aaa att gtg gtt aaa tca gag Lys Phe Asn Ser Asn Ile Ile Gly Asn Lys Ile Val Val Lys Ser Glu 590 595 600	1946
gtt gtg aat gga cga tat gcg ctg gat caa gga ttg gtc ctt gaa aag Val Val Asn Gly Arg Tyr Ala Leu Asp Gln Gly Leu Val Leu Glu Lys 605 610 615 620	1994
gtg aca tta ttg gga ttt gaa aat gtg aga gga ttg aag agc tat gag Val Thr Leu Leu Gly Phe Glu Asn Val Arg Gly Leu Lys Ser Tyr Glu 625 630 635	2042
ctt gtt gga tca cac cag caa ggg aac aca aca atg aag gaa agt ctt Leu Val Gly Ser His Gln Gln Gly Asn Thr Thr Met Lys Glu Ser Leu 640 645 650	2090
aag cag agt gga cag ttt gtt act atg gaa atc tca ggg atg tca ata Lys Gln Ser Gly Gln Phe Val Thr Met Glu Ile Ser Gly Met Ser Ile 655 660 665	2138
ttg ata ggg aaa gag ttc aaa ttg gag cta tac atc att act Leu Ile Gly Lys Glu Phe Lys Leu Glu Leu Tyr Ile Ile Thr 670 675 680	2180
taacaaatga attaagttat atacgcttgt tgtatgaaat ttctttcat ttatcaatgc agttaattt atgataaaaa aaaaaaaaaaa aa	2240 2272

<210> 2
<211> 682
<212> PRT
<213> Solanum tuberosum

<400> 2

Pro Lys Leu Arg Pro Arg Val His Pro Ser Gln·His His Pro Ile Gln 1 5 10 15
--

Leu His Arg Pro Pro Ala Leu His Arg Gly Tyr Ser Phe Arg Tyr Phe 20 25 30

Ala Gly Val Ser His Gly Val Leu Leu Leu Ser Ser Asn Gly Met Asp
35 40 45

Ile Val Tyr Thr Gly Asp Arg Ile Ser Tyr Lys Val Ile Gly Gly Leu
50 55 60

Ile Asp Leu Tyr Phe Phe Ala Gly Pro Ser Pro Glu Met Val Val Asp
65 70 75 80

Gln Tyr Thr Gln Leu Ile Gly Arg Pro Ala Ala Met Pro Tyr Trp Ser
85 90 95

Phe Gly Phe His Gln Cys Arg Trp Gly Tyr Lys Asn Ile Asp Asp Val
100 105 110

Glu Leu Val Val Asp Ser Tyr Ala Lys Ser Arg Ile Pro Leu Glu Val
115 120 125

Met Trp Thr Asp Ile Asp Tyr Met Asp Gly Phe Lys Asp Phe Thr Leu
130 135 140

Asp Pro Val Asn Phe Pro Leu Glu Arg Val Ile Phe Phe Leu Arg Lys
145 150 155 160

Leu His Gln Asn Asp Gln Lys Tyr Val Leu Ile Val Asp Pro Gly Ile
165 170 175

Ser Ile Asn Asn Thr Tyr Asp Thr Tyr Arg Arg Gly Met Glu Ala Asp
180 185 190

Val Phe Ile Lys Arg Asp Asn Met Pro Tyr Gln Gly Val Val Trp Pro
195 200 205

Gly Asn Val Tyr Tyr Pro Asp Phe Leu Asn Pro Ala Thr Glu Val Phe
210 215 220

Trp Arg Asn Glu Ile Glu Lys Phe Gln Asp Leu Val Pro Phe Asp Gly
225 230 235 240

Leu Trp Leu Asp Met Asn Glu Leu Ser Asn Phe Ile Thr Ser Pro Pro
245 250 255

Thr Pro Ser Ser Thr Phe Asp Asp Pro Pro Tyr Lys Ile Asn Asn Ser

260

265

270

Gly Asp His Leu Pro Ile Asn Tyr Arg Thr Val Pro Ala Thr Ser Thr
275 280 285

His Phe Gly Asp Thr Met Glu Tyr Asn Val His Asn Leu Tyr Gly Leu
290 295 300

Leu Glu Ser Arg Ala Thr Tyr Ser Ala Leu Val Asn Val Thr Gly Lys
305 310 315 320

Arg Pro Phe Ile Leu Val Arg Ser Thr Phe Leu Gly Ser Gly Arg Tyr
325 330 335

Thr Ser His Trp Thr Gly Asp Asn Ala Ala Thr Trp Asn Asp Leu Ala
340 345 350

Tyr Ser Ile Pro Thr Ile Leu Ser Phe Gly Leu Phe Gly Ile Pro Met
355 360 365

Val Gly Ala Asp Ile Cys Gly Phe Ser Ser Asn Thr Thr Glu Glu Leu
370 375 380

Cys Arg Arg Trp Ile Gln Leu Gly Ala Phe Tyr Pro Phe Ala Arg Asp
385 390 395 400

His Ser Ala Lys Asp Thr Thr Pro Gln Glu Leu Tyr Ser Trp Asp Ser
405 410 415

Val Ala Ala Ala Lys Lys Val Leu Gly Leu Arg Tyr Gln Leu Leu
420 425 430

Pro Tyr Phe Tyr Met Leu Met Tyr Glu Ala His Ile Lys Gly Thr Pro
435 440 445

Ile Ala Arg Pro Leu Phe Phe Ser Phe Pro Gln Asp Ala Lys Thr Phe
450 455 460

Asp Ile Ser Thr Gln Phe Leu Leu Gly Lys Gly Val Met Ile Ser Pro
465 470 475 480

Ile Leu Lys Gln Gly Ala Thr Ser Val Asp Ala Tyr Phe Pro Ala Gly
485 490 495

Asn Trp Phe Asp Leu Phe Asn Tyr Ser Arg Ser Val Ser Leu Asn Gln
500 505 510

Gly Thr Tyr Met Thr Leu Asp Ala Pro Pro Asp His Ile Asn Val His
515 520 525

Val Arg Glu Gly Asn Ile Leu Val Met Gln Gly Glu Ala Met Thr Thr
530 535 540

Gln Ala Ala Gln Arg Thr Ala Phe Lys Leu Leu Val Val Leu Ser Ser
545 550 555 560

Ser Lys Asn Ser Thr Gly Glu Leu Phe Val Asp Asp Asp Asp Glu Val
565 570 575

Gln Met Gly Arg Glu Gly Gly Arg Trp Thr Leu Val Lys Phe Asn Ser
580 585 590

Asn Ile Ile Gly Asn Lys Ile Val Val Lys Ser Glu Val Val Asn Gly
595 600 605

Arg Tyr Ala Leu Asp Gln Gly Leu Val Leu Glu Lys Val Thr Leu Leu
610 615 620

Gly Phe Glu Asn Val Arg Gly Leu Lys Ser Tyr Glu Leu Val Gly Ser
625 630 635 640

His Gln Gln Gly Asn Thr Thr Met Lys Glu Ser Leu Lys Gln Ser Gly
645 650 655

Gln Phe Val Thr Met Glu Ile Ser Gly Met Ser Ile Leu Ile Gly Lys
660 665 670

Glu Phe Lys Leu Glu Leu Tyr Ile Ile Thr
675 680

SEQUENCE LISTING

<110> Hoechst Schering AgrEvo GmbH

<120> Nucleic acid molecules encoding an α -glucosidase, plants which synthesize a modified starch, the generation of the plants, their use, and the modified starch

<400> 1

CGAATACGAA	TAACCGACGC	TAACCATCAA	CGATGGGAAG	TGCCGGAAGA	AATTCTCCAC	60
CGTCCACCAAC	CGCGCGTCGCC	GCCGTCRAACC	TCCAACCTCCT	CATCAGAAAAA	CCACTCCCCA	120
ATTACCCCTCT	CTAACCCRAA	CTCAGACCTA	GAGTTACCCC	TTCACAACAC	CATCCCATTC	180
AGCTTCACCG	TCCGGCGCG	CTCCACCGGG	GATACTCTTT	TCGATACTTC	GCCGGAGTTA	240
GTCATGGGGT	TTTCCCTCTG	AGTAGCAATG	GCATGGATAT	TGTGTATAACG	GTCATAGGA	300
TTAGTTACAA	GGTGATTGGA	CGGTTAATTG	ATTTGTATTI	CTTTCGCGGA	CCTTCGCGGG	360
AAATGGTGGT	GGATCACTAT	ACTCAGCTTA	TTGGTCGTCC	TGCTGCTATG	CCATATTGGT	420
CTTTCGGATT	TCACCAATGC	CGGTGGGGTT	ACAAGAATAT	TGATGATGTT	GAACGGTAG	480
TGGATAGTTA	TGCAAAGTCT	AGAATAACCGC	TGGAGGTTAT	GTGGACTGAT	ATTGATTACA	540
TGGATGGTTT	TAAGGACTTC	ACACTCGATC	CAGTTAACTT	CCCACCTGGAG	CGGGTAATTI	600
TTTTTCTCAG	GAAGCTTCAT	CAGAATGATC	AGAAATATGT	ACTAATAGTA	GATCCAGGAA	660
TTAGCATCAA	CAATACATAT	GACACCTATA	GGAGAGGCAT	GGAAGCAGAT	GTCTTCATAA	720
AACGCGATAA	TATGCCCTAC	GAAGGGGTIG	TTTCGCCAGG	GAATGTTTAT	TATCCTGATT	780
TTCTAAATCC	AGCTACTGAA	GTATTTTGGA	GAAATGAAAT	TGAGAAGTTC	CAGGATCTCG	840
TACCTTTGAA	TGGCCTGTGG	CTTGACATGA	ATGAATTGTC	AAACTTCATA	ACTTCCCCTC	900

per
page
#3

CTACACCATIC ATCTACCTTT GATGATCCTC CCTACAGAT AAACAACCTCT GGCGATCACT 960
 TGCCCATCAA TTATAGAACAA GTTCCAGCCA CTTCTACACA TTTTGGTGAT ACAATGGAGT 1020
 ATAATGTCCA TAACCTTTAT GGATTACTTG AATCTAGAGC CACTTATAGT GCATTGGTTA 1080
 ATGTCACTGG TAAAAGGCCA TTCATTCTTG TAAGATCACAC TTTTCTGGC TCTGGCAGAT 1140
 ACACGTCACA TTGGACTGGA GATAATGCTG CTACCTGGAA CGATTTGGCA TACTCCATTC 1200
 CTACTATCTT GAGCTTTGGA TTGTTGGAA TTCCAATGGT TGGAGCTGAT ATATGTGGTT 1260
 TTTCAGTAA CACTACTGAA GAGCTTGCC GCGGCTGGAT TCAGCTGGA GCATTCTATC 1320
 CATTGCAAG AGACCACTCT GCTAAGGACA CAACCCCCCA AGAGCTCTAT AGTTGGGATT 1380
 CAGTTGCTGC AGCAGCCAAG AAAGTCCTTG GGCTCCGATA TCAGTTACTT CCATACTTTT 1440
 ATATGCTTAT GTACGGAGGCA CATATAAAAG GGACTCCCCT TGCAAGGACCC CTCTTCTTCT 1500
 CTTTCCCTCA AGATGCCAAG ACATTTGATA TCAGGCACACA GTTCCCTCTC GGTAAAGGTG 1560
 TCATGATCTC ACCTATACTT AACGAAGGAG CRACCTCTGT TGATGCATAT TTCCCTGCTG 1620
 GAAACTGGTT TGACCTCTTC AATTACTCTC CCTCTGTGAG TTTGAATCAA GGAACATATA 1680
 TGACACTTGA CGCACCCACCA GATCATATAA ATGTACATGT TCGTGAAGGG AACATATTGG 1740
 TCATGCAAGG GGAAGGCTATG ACAACACAG CTGCTCAGAG GACTGCATTC AAACCTCTT 1800
 TCGTGCTGAG CAGCACCAAA AACAGCACAG GAGAACTATT TGTGGACGAT GACGGATGRGG 1860
 TGCAGATGGG AAGAGAGGGA GGGAGGTGGA CGCTAGTTAA GTTAAACAGC AATATCATTG 1920
 GCAATAAAAT TGTGGTTAAA TCAGAGGTG TGAAATGGACG ATATGCGCTG GATCAAGGAT 1980
 TGGTCTTCA AAGGGTGACA TTATTGGGAT TTGAAAATGT GAGAGGATTG AAGAGCTATG 2040
 AGCTTGTGAG ATCACACCAAG CAAGGGAAACA CAACAATGAA GGAAAGTCTT AAGCAGAGTG 2100
 GACAGTTTGT TACTATGGAA ATCTCAGGGAA TGTCAATATT GATAGGGAAA GAGTTCAAAT 2160
 TGGAGCTATA CATCATTACT TAACAAATGA ATTAAGTTAT ATACGCTTGT TGTATGAAAT 2220
 TTTCTTTCAT TTATCAATGC AGTTAAATTG ATGATAAAAAA AAAAAAAAAAA AA 2272

- <210> 2
- <211> 682
- <212> PRT
- <213> S. tuberosum

<400> 2

Pro Lys Leu Arg Pro Arg Val His Pro Ser Gln His His Pro Ile Gln
1 5 10 15

Leu His Arg Pro Pro Ala Leu His Arg Gly Tyr Ser Phe Arg Tyr Phe
20 25 30

Ala Gly Val Ser His Gly Val Leu Leu Ser Ser Asn Gly Met Asp
35 40 45

Ile Val Tyr Thr Gly Asp Arg Ile Ser Tyr Lys Val Ile Gly Gly Leu
50 55 60

Ile Asp Leu Tyr Phe Phe Ala Gly Pro Ser Pro Glu Met Val Val Asp
65 70 75 80

Gln Tyr Thr Gln Leu Ile Gly Arg Pro Ala Ala Met Pro Tyr Trp Ser
85 90 95

Phe Gly Phe His Gln Cys Arg Trp Gly Tyr Lys Asn Ile Asp Asp Val
100 105 110

Glu Leu Val Val Asp Ser Tyr Ala Lys Ser Arg Ile Pro Leu Glu Val
115 120 125

Met Trp Thr Asp Ile Asp Tyr Met Asp Gly Phe Lys Asp Phe Thr Leu
130 135 140

Asp Pro Val Asn Phe Pro Leu Glu Arg Val Ile Phe Phe Leu Arg Lys
145 150 155 160

Leu His Gln Asn Asp Gln Lys Tyr Val Leu Ile Val Asp Pro Gly Ile
165 170 175

Ser Ile Asn Asn Thr Tyr Asp Thr Tyr Arg Arg Gly Met Glu Ala Asp
180 185 190

Val Phe Ile Lys Arg Asp Asn Met Pro Tyr Gln Gly Val Val Trp Pro
195 200 205

Gly Asn Val Tyr Tyr Pro Asp Phe Leu Asn Pro Ala Thr Glu Val Phe
210 215 220

Trp Arg Asn Glu Ile Glu Lys Phe Gln Asp Leu Val Pro Phe Asp Gly
 225 230 235 240
 Leu Trp Leu Asp Met Asn Glu Leu Ser Asn Phe Ile Thr Ser Pro Pro
 245 250 255
 Thr Pro Ser Ser Thr Phe Asp Asp Pro Pro Tyr Lys Ile Asn Asn Ser
 260 265 270
 Gly Asp His Leu Pro Ile Asn Tyr Arg Thr Val Pro Ala Thr Ser Thr
 275 280 285
 His Phe Gly Asp Thr Met Glu Tyr Asn Val His Asn Leu Tyr Gly Leu
 290 295 300
 Leu Glu Ser Arg Ala Thr Tyr Ser Ala Leu Val Asn Val Thr Gly Lys
 305 310 315 320
 Arg Pro Phe Ile Leu Val Arg Ser Thr Phe Leu Gly Ser Gly Arg Tyr
 325 330 335
 Thr Ser His Trp Thr Gly Asp Asn Ala Ala Thr Trp Asn Asp Leu Ala
 340 345 350
 Tyr Ser Ile Pro Thr Ile Leu Ser Phe Gly Leu Phe Gly Ile Pro Met
 355 360 365
 Val Gly Ala Asp Ile Cys Gly Phe Ser Ser Asn Thr Thr Glu Glu Leu
 370 375 380
 Cys Arg Arg Trp Ile Gln Leu Gly Ala Phe Tyr Pro Phe Ala Arg Asp
 385 390 395 400
 His Ser Ala Lys Asp Thr Thr Pro Gln Glu Leu Tyr Ser Trp Asp Ser
 405 410 415
 Val Ala Ala Ala Ala Lys Lys Val Leu Gly Leu Arg Tyr Gln Leu Leu
 420 425 430
 Pro Tyr Phe Tyr Met Leu Met Tyr Glu Ala His Ile Lys Gly Thr Pro
 435 440 445
 Ile Ala Arg Pro Leu Phe Phe Ser Phe Pro Gln Asp Ala Lys Thr Phe
 450 455 460
 Asp Ile Ser Thr Gln Phe Leu Leu Gly Lys Gly Val Met Ile Ser Pro
 465 470 475 480
 Ile Leu Lys Gln Gly Ala Thr Ser Val Asp Ala Tyr Phe Pro Ala Gly
 485 490 495
 Asn Trp Phe Asp Leu Phe Asn Tyr Ser Arg Ser Val Ser Leu Asn Gln
 500 505 510

Gly Thr Tyr Met Thr Leu Asp Ala Pro Pro Asp His Ile Asn Val His
515 520 525

Val Arg Glu Gly Asn Ile Leu Val Met Gln Gly Glu Ala Met Thr Thr
530 535 540

Gln Ala Ala Gln Arg Thr Ala Phe Lys Leu Leu Val Val Leu Ser Ser
545 550 555 560

Ser Lys Asn Ser Thr Gly Glu Leu Phe Val Asp Asp Asp Glu Val
565 570 575

Gln Met Gly Arg Glu Gly Gly Arg Trp Thr Leu Val Lys Phe Asn Ser
580 585 590

Asn Ile Ile Gly Asn Lys Ile Val Val Lys Ser Glu Val Val Asn Gly
595 600 605

Arg Tyr Ala Leu Asp Gln Gly Leu Val Leu Glu Lys Val Thr Leu Leu
610 615 620

Gly Phe Glu Asn Val Arg Gly Leu Lys Ser Tyr Glu Leu Val Gly Ser
625 630 635 640

His Gln Gln Gly Asn Thr Thr Met Lys Glu Ser Leu Lys Gln Ser Gly
645 650 655

Gln Phe Val Thr Met Glu Ile Ser Gly Met Ser Ile Leu Ile Gly Lys
660 665 670

Glu Phe Lys Leu Glu Leu Tyr Ile Ile Thr
675 680